

RAW SEQUENCE LISTING

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Application Serial Number: 10/784,513
Source: IFWJ
Date Processed by STIC: 3/20/2006

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/784,513DATE: 03/20/2006
TIME: 12:29:15

INPUT SET: S30786.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>
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1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Gorski, David H.
6 Walsh, Kenneth
7
8 (ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene
9
10 (iii) NUMBER OF SEQUENCES: 19
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Calfee, Halter, and Griswold
14 (B) STREET: 800 Superior Avenue
15 (C) CITY: Cleveland
16 (D) STATE: Ohio
17 (E) COUNTRY: U.S.A.
18 (F) ZIP: 44114-2688
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:US/10/784,513
28 (B) FILING DATE: 23-FEB-2004
29 (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER:US/08/203,532
31 (B) FILING DATE: 24-FEB-1994
32 (C) CLASSIFICATION:435
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Golrick, Mary E.
36 (B) REGISTRATION NUMBER: 34829
37 (C) REFERENCE/DOCKET NUMBER: 22311/00114
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (216) 622-8200
41 (B) TELEFAX: (216) 241-0816
42 (C) TELEX: 980499
43
44
45 (2) INFORMATION FOR SEQ ID NO:1:
46

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 2244 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: both
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: cDNA
54
55      (iii) HYPOTHETICAL: NO
56
57      (iv) ANTI-SENSE: NO
58
59
60      (ix) FEATURE:
61          (A) NAME/KEY: CDS
62          (B) LOCATION: 197..1108
63
64
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67      GTCAAGTGTT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT      60
68
69      CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT      120
70
71      AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGAAG      180
72
73      CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC      229
74          Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
75          1 5 10
76
77      CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG      277
78      Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu
79          15 20 25
80
81      GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA      325
82      Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
83          30 35 40
84
85      TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG      373
86      Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
87          45 50 55
88
89      TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC      421
90      Phe Ala Ser Gln His His Arg Gly His His His His His His His His
91          60 65 70 75
92
93      CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG      469
94      His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp
95          80 85 90
96
97      CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT      517
98      His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
99          95 100 105

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101	TGC	CTG	CAG	CCT	GAT	TCC	GGA	GGG	CCC	CCG	GAG	CTG	GGG	AGC	AGC	CCT		565
102	Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro		
103			110					115					120					
104																		
105	CCG	GTC	CTG	TGC	TCC	AAC	TCT	TCT	AGC	CTG	GGC	TCC	AGC	ACC	CCG	ACC		613
106	Pro	Val	Leu	Cys	Ser	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr		
107		125					130					135						
108																		
109	GGA	GCC	GCG	TGC	GCA	CCA	AGG	GAT	TAT	GGC	CGT	CAA	GCG	CTG	TCA	CCC		661
110	Gly	Ala	Ala	Cys	Ala	Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro		
111	140					145					150					155		
112																		
113	GCA	GAA	GTG	GAG	AAG	AGA	AGT	GGC	AGC	AAA	AGA	AAA	AGC	GAC	AGT	TCA		709
114	Ala	Glu	Val	Glu	Lys	Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser		
115					160					165					170			
116																		
117	GAT	TCC	CAG	GAA	GGA	AAT	TAC	AAG	TCA	GAA	GTG	AAC	AGC	AAA	CCT	AGG		757
118	Asp	Ser	Gln	Glu	Gly	Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg		
119			175					180						185				
120																		
121	AGG	GAA	AGA	ACA	GCT	TTC	ACC	AAA	GAG	CAA	ATC	AGA	GAA	CTT	GAG	GCA		805
122	Arg	Glu	Arg	Thr	Ala	Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala		
123			190					195					200					
124																		
125	GAG	TTC	GCC	CAT	CAT	AAC	TAT	CTG	ACC	AGA	CTG	AGA	AGA	TAT	GAG	ATA		853
126	Glu	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile		
127		205					210					215						
128																		
129	GCG	GTG	AAC	CTA	GAC	CTC	ACT	GAA	AGA	CAG	GTG	AAA	GTG	TGG	TTC	CAG		901
130	Ala	Val	Asn	Leu	Asp	Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln		
131	220					225					230					235		
132																		
133	AAC	AGG	AGA	ATG	AAG	TGG	AAG	CGG	GTC	AAG	GGG	GGA	CAA	CAA	GGA	GCT		949
134	Asn	Arg	Arg	Met	Lys	Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala		
135					240					245					250			
136																		
137	GCA	GCC	CGA	GAA	AAG	GAA	CTG	GTG	AAT	GTG	AAA	AAG	GGA	ACA	CTT	CTT		997
138	Ala	Ala	Arg	Glu	Lys	Glu	Leu	Val										

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153 ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTG 1205
154
155 CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC 1265
156
157 ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA 1325
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159 AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTTGG CTTGCACTGA 1385
160
161 AAATTAAATT GCTACCAAGA GCAAACCTCG TAAGACATTT TGA CTCAAGT TGTCTCCAGA 1445
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163 GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC 1505
164
165 TGGGCAGGTA TTTGCTTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA 1565
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167 AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG 1625
168
169 AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTTT AGCAAATGCA 1685
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171 TTCATATTAG CTGATGAAAA TAGGCTTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT 1745
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173 TTTATACATT TTTTGTGTCAG TCAGAGACAT CAGTATGTGC TTA CTGTGT TCAAGTAGAG 1805
174
175 GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG 1865
176
177 TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC 1925
178
179 TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA 1985
180
181 GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAACTG TTAATGGTAT GTGTCTGCTT 2045
182
183 CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA 2105
184
185 CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA 2165
186
187 AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA 2225
188
189 AAAAAAAGTT AAATAAATG 2244

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

203 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
204 1 5 10 15
205

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206	Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
207	20 25 30
208	
209	Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys
210	35 40 45
211	
212	Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
213	50 55 60
214	
215	His Arg Gly His His His His His His His His His His His His His Gln
216	65 70 75 80
217	
218	Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
219	85 90 95
220	
221	Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
222	100 105 110
223	
224	Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
225	115 120 125
226	
227	Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
228	130 135 140
229	
230	Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
231	145 150 155 160
232	
233	Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
234	165 170 175
235	
236	Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Arg Glu Arg Thr Ala
237	180 185 190
238	
239	Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
240	195 200 205
241	
242	Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
243	210 215 220
244	
245	Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
246	225 230 235 240
247	
248	Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
249	245 250 255
250	
251	Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
252	260 265 270
253	
254	Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
255	275 280 285
256	
257	Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
258	290 295 300

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/10/784,513

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Line	Error	Original Text
32	Wrong Classification	(C) CLASSIFICATION:435